

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: August 9, 2002, 20:02:52 ; Search time 16.71 Seconds
(without alignments) 598.043 Million cell updates/sec

Title: US-09-622-613a-2
Perfect score: 576
Sequence: 1 ODWLTFQKKHLNTRDVCN.....TFCVTCENQAPVHFVGVGHC 104

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283138 seqs, 96089334 residues

Total number of hits satisfying chosen parameters: 283138

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database :
1: p1r1:*
2: p1r2:*
3: p1r3:*
4: p1r4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length DB	ID	Description
1	544	94.4	104	2 A39035	ribonuclease-relat
2	288	50.0	111	2 A27121	ribonuclease-relat
3	284.5	49.4	111	1 JX0120	ribonuclease-relat
4	268.5	46.6	111	2 JX0085	pancreatic ribonuc
5	154	26.7	119	2 S41111	pancreatic ribonuc
6	128	22.2	124	1 NRUI	pancreatic ribonuc
7	125	21.7	128	1 NRGPB	pancreatic ribonuc
8	124	21.5	125	1 A32474	angiotensin [valida
9	123	21.4	128	1 NRCU	pancreatic ribonuc
10	122	21.2	124	1 NRMHK	pancreatic ribonuc
11	121	21.0	128	1 NRKS	pancreatic ribonuc
12	118.5	20.6	145	1 A35932	angiotensin precus
13	117	20.3	124	1 NRPB	pancreatic ribonuc
14	116.5	20.2	147	2 T52489	ribonuclease 4 (EC
15	116	20.1	125	1 E43825	angiotensin - rabdi
16	114	19.8	124	1 NRCB	pancreatic ribonuc
17	113.5	19.7	155	2 JX0159	angiotensin precus
18	113	19.6	128	1 NRY	pancreatic ribonuc
19	112	19.4	147	1 NRUHG	angiotensin precus
20	111	19.3	124	1 NRHP	pancreatic ribonuc
21	111	19.3	156	2 JX0160	angiotensin associa
22	109.5	19.0	123	1 A43825	angiotensin - pig
23	109	18.9	124	1 NRCB	pancreatic ribonuc
24	109	18.9	124	1 JX0560	pancreatic ribonuc
25	109	18.9	150	1 NRBO	pancreatic ribonuc
26	108	18.8	124	2 S08549	ribonuclease - dom
27	108	18.8	128	1 NRHO	pancreatic ribonuc
28	108	18.8	128	1 NRPO	pancreatic ribonuc
29	108	18.8	167	2 S20066	pancreatic-type ri

30	106	18.4	124	1 NRSH	pancreatic ribonuc
31	106	18.4	124	1 NRPR	pancreatic ribonuc
32	106	18.4	124	1 NRGPA	pancreatic ribonuc
33	106	18.4	124	2 S07141	pancreatic ribonuc
34	105	18.2	124	1 NRCB	pancreatic ribonuc
35	105	18.2	124	1 NRCN	pancreatic ribonuc
36	104.5	18.1	119	2 JX0115	pancreatic ribonuc
37	104.5	18.1	122	1 NRKGR	pancreatic ribonuc
38	104	18.1	124	1 NRGF	pancreatic ribonuc
39	102.5	17.8	147	2 A53180	ribonuclease P13 (
40	102	17.7	124	1 NRDBO	pancreatic ribonuc
41	102	17.7	124	1 NRCM	pancreatic ribonuc
42	102	17.7	124	1 NRCM	pancreatic ribonuc
43	102	17.7	124	1 NRCM	pancreatic ribonuc
44	102	17.7	128	1 NRCW2	pancreatic ribonuc
45	101	17.5	124	1 NRHY	pancreatic ribonuc

ALIGNMENTS

RESULT 1
A39035
ribonuclease-related anti-tumor protein - northern leopard frog (fragment)
C:Species: Rana pipiens (northern leopard frog)
C:Date: 31-Jul-1991 #sequence_revision 31-Jul-1991 #text_change 30-Jun-1993
C:Accession: A39035
R:Ardelet, W.; Mikulski, S.M.; Shogen, K.
J. Biol. Chem. 266, 245-251, 1991
A:Title: Amino acid sequence of an anti-tumor protein from Rana pipiens oocytes and e
A:Reference number: A39035; MUID:91093131
A:Accession: A39035
A:Status: preliminary
A:Molecule type: protein
A:Residues: 1-104 <ARD>
C:Superfamily: pancreatic ribonuclease

Query Match 94.4%; Score 544; DB 2; Length 104;
Best Local Similarity 94.2%; Pred. No. 7.5e-45;
Matches 98; Conservative 3; Mismatches 3; Indels 0; Gaps 0;
Oy 1 ODWLTFQKKHLNTRDVCNINIMSTNLFPHCKDKNTFIYSRPEPVKAICKGIASKNVLT 60
Db 1 EDWLTFQKKHLNTRDVCNIMSTNLFPHCKDKNTFIYSRPEPVKAICKGIASKNVLT 60
Oy 61 SEFYISDCNVTSPCKYKLRKSTNFCVTCENQAPVHFVGVGHC 104
Db 61 SEFYISDCNVTSPCKYKLRKSTNFCVTCENQAPVHFVGVGSC 104

RESULT 2
A27121
ribonuclease-related sialic acid-binding lectin - bullfrog
C:Species: Rana catesbeiana (bullfrog)
C:Date: 19-Nov-1988 #sequence_revision 19-Nov-1988 #text_change 30-Jun-1993
R:Tilani, K.; Takio, K.; Kuwada, M.; Nitte, K.; Sakakibara, F.; Kawachi, H.; Takayan
Biochemistry 26, 2189-2194, 1987
A:Title: Amino acid sequence of sialic acid-binding lectin from frog (Rana catesbeiana
A:Reference number: A27121; MUID:87299649
A:Accession: A27121
A:Molecule type: protein
A:Residues: 1-111 <TIT>
C:Superfamily: pancreatic ribonuclease
C:Keywords: lectin

Query Match 50.0%; Score 288; DB 2; Length 111;
Best Local Similarity 48.6%; Pred. No. 1.5e-22;
Matches 54; Conservative 17; Mismatches 32; Indels 8; Gaps 3;
Oy 1 ODWLTFQKKHLNTRDVCNINIMSTNLF---HCKDKNTFIYSRPEPVKAICKGIASKN 56

```
Db      1 EMWAFPOQKHINTPIINCNTIMDNINIIYVGQCRRVNFIFISSATVTAKICTGVI -NMN   59
        ::|||:::|||:::|||:::|||:::|||:::|||:::|||:::|||:::|||:::|||
Oy      57 VLTTFSEFLSDC---NWTSRPCKRYKLKSTNSTFECYTCENQAPVHHEGVGHIC 104
        |||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
Dd      60 VLSTRFDLNTCTRTSIIRPCPPYSRTEPNICYKCENQYPFHAGIGRC 110
        |||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||

RESULT    3
JX0120
ribonuclease-related sialic acid-binding lectin - Japanese frog
C:Species: Rana japonica (Japanese frog)
C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
C:Accession: JX0120
R:Kamiya, Y.: Oiyama, F.; Oyama, R.; Sakakibara, F.; Nitta, K.; Kawachi, H.; Takayanagi, T. Biochem. 108, 139-143, 1990
A>Title: Amino acid sequence of a lectin from Japanese frog (Rana japonica) eggs.
```

A:Accession: JX0120
A:Molecule type: protein
A:Residues: 1-111 <RAM>
A:Experimental source: egg
C:Superfamily: pancreatic ribonuclease
C:Keywords: lectin; pyroglyutamic acid
E:1,Modified site: pyroglutidone carboxylic acid (Gln) #status experimental
E:19-72,34-82,52-97,94-111/Disulfide bonds: #status experimental

Query Match	49.4%	Score 284.5	DB 1	Length 111
Best Local Similarity	45.0%	Pred. No. 3.5e-22		
Matches 50	Conservative 19	Mismatches 35	Indels 7	Gaps 2

```
QY      1 QDWLFQQKKHLNTRDVDCNIIMSNLE----HCKDANTFYISREPEVAICIGLIASKN   56  
       |:| :||: |:::||| || ::| :||||| | |||| | :||  
Db      1 QNWAKFOEKHIPTNSINCNTIMDKSIYIVGGQKERNTFISSATTVKAICSGASTNRN   60
```

```

Oy  57 VLTTSBFYLSDC---NVTSRPCKYKLLKSTNTFCVYGCENQAPYHVEVGHC 104
    ||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db  61 VLSTTFQQLNTCLRSATAPRPCPYNSRTETNVICVKENRLPHEFAGISGC 111

```

RESULT 4
JX0085
pancreatic ribonuclease (EC 3.1.27.5) - bullfrog
C:Species: Rana catesbeiana (bullfrog)
C:Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 05-Aug-1994
C:Accession: JX0085
R:Nita, R.; Katayama, N.; Okabe, Y.; Iwana, M.; Watanabe, H.; Abe, Y.; Okazaki, T.; Ohn
J. Biochem 106, 729-735, 1989
A:Title: Primary structure of a ribonuclease from bullfrog (Rana catesbeiana) liver.
A:Reference number: JX0085; MUID:90130374

A: Molecule type: protein
 A: Residues: 1-111 <NTP>
 C: Superfamily: pancreatic ribonuclease
 E: Modified site: pyroglutamic acid
 F:1 Modified site: pyrrolidone carboxylic acid (Gln) #status experimental
 F:10-35,104/Active site: His, Lys, His #status predicted
 F:10-73,34-82,52-97,94-111/Disulfide bonds: #status predicted

Query Match	46.6%	Score 268.5	DB 2	Length 111
Best Local Similarly	43.2%	Pred. No. 1.5e-20		
Matches 48	Conservative 19	Mismatches 37	Indels 7	Gaps 2

```
Qy      1 QDWLTFOKKHLNTRDVDCNIIMSNLF----HCKDKNTFIYSRPEPVKAICGGIASKN 560
        | :|::||: ||::||| | |::||| | |::||| | |::||| | |::||| |
Db      1 QNMAREKEKHIFSTSSIDCNTIMDKAIYIVGCGKCKERMTFLISSEDNVAKIACSGVSPDRK 600
```

```
QY      57 VLTTSEFLSDC---NYSRPPCKYKLLKKSSINTFCVTCENAPVHFEVGVC 104
          |::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db      61 ELSTSFELNTCIDRSITPRPCPYHPSPDNKKICVKCEQLPVHFVGIGKC 111
```

RESULT 5
S4111
pancreatic ribonuclease - common iguana
C:Species: Iguana iguana (common iguana)
C:Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 21-Aug-1998
C:Accession: S4111
R:Zhao, W.; Beintema, J. J.; Hofsteenge, J.
Eur. J. Biochem. 219, 641-646, 1994
A:Title: The amino acid sequence of iguana (Iguana iguana) pancreatic ribonuclease
A:Reference number: S4111; MUID:94139745
A:Accession: S4111
A:Status: preliminary
A:Molecule type: protein
A:Residues: 1-119 <ZHA>
C:Superfamily: pancreatic ribonuclease

Query Match	26.7%	Score 154	DB 2	Length 119
Best Local Similarity	30.7%	Pred. No. 9.4e-09		
Matches 35	Conservative 20	Mismatches 43	Indels 16	Gaps 5

```

QY      1 QDWLTFQKKHL-----INTRDVONIIIM---STNLEHCKDKDKTFTVYSRPEPVKAIC-K 49
      111 :11111:      : :1::1      : 11 :111::1      : : :1
Db      1 QDWSSTQNKHIDYPTETASNPNAVCYCDLMQRRNLNPTKCKTRNTFVHASPSEIOVCGSG 600

```

Oy 50 GIATSKNVLTTSE-FYLSDC---NVTSRPCKKYLKSTNFECVTCENAPVHF 98
| : :: | : || | : || |
Db 61 GTHYEDNLVSNSFIDLTDCKNVGSTAPSSCKYNPTGTRIRIACENNQPVHF 114

```

RESULT      6
NRUI
pancreatic ribonuclease (EC 3.1.27.5) - cufs
N:Alternate names: RNase 1; RNase A
C:Species: Galea musteloides (cufs)
C>Date: 03-Aug-1984 #sequence_revision 03-Aug-1984 #text_change 04-Oct-1996
C:Accession: A00827
R:Belintema, J.-J.; Neuteboom, B.
J Mol. Evol. 19, 145-152, 1983
A:Title: Origin of the duplicated ribonuclease gene in guinea pig: comparison of the
A:Reference number: A92957; MUID: 87036770

```

A:NGRACDSS: 129 BLA
A:Note: about one-third of the molecules lacked Ala-1
C:Comment: The culs is a rodent belonging to the same subfamily as the guinea pig
C:Superfamily: pancreatic ribonuclease
C:Keywords: glycoprotein; hydrolysis; nucleic acid digestion; pancreas
F:12,41,119/Active site: His_Lys, His #status predicted
F:26-84,40-95,58-110,65-72/Disulfide bonds: #status predicted
F:94/Binding site: carbohydrate (asn) (covalent) #status absent

Query Match	22.2%	Score	128:	DB 1:	Length	124:			
Best Local Similarity	30.6%	Pred. NO.	4.6e-06:						
Matches	37:	Conservative	18:	Mismatches	34:	Indels	32:	Gaps	7:

```
Oy      4  LTFQKKHL-----TNPTRDVDCNIIIM---STNLFHKDKDNFTIYSRPEVKAIGKIIA 53
      :  :::::  |||  ||  ||  |||  :  ||:::  :
Db      6  MKFQQRHMDSDCHPDTNITN--YCNEMMVRNRSMTQGRCKPVPNTEVHERLEAVQAVC---S 59
```

QY 54 SKNV-----LTTSEFLSDCANTSRP-----CKYKLLKSTNYFCVGCEN--QAPVH 97
 ||| :| :||| ||| |::: :| ||| |||
 Db 60 QKNVFCCKNGQTCNYQSHSSMRITDCRATYSSSKYPCNCSTYMTQAOAKSIIVACEGTPSPVPH 119

QY	98	F	98
Db	120	F	120

RESULTS

A:Accession: A324/4
A:Molecule type: protein
A:Residues: 1-125 <BON>
A:Experimental source: Plasma
R:Maes, P.; Damart, D.; Rommens, C.; Montreuil, J.; Spik, G.; Tartar, A.
FEBS Lett. 241, 41-45, 1988
A:Title: The complete amino acid sequence of bovine milk angiotensin.
A:Reference number: S02001; MUID:89065101
A:Accession: S02001
A:Molecule type: protein
A:Residues: 1-125 <MAE>
A:Experimental source: milk
R:Chachaya, K.R.; Shapiro, R.; Riordan, J.F.; Vallee, B.L.
submitted to the Brookhaven Protein Data Bank, January 1995
A:Reference number: A65065; PDB:1AG1
A:Contents: annotation; X-ray crystallography, 1.5 angstroms, residues 1-125
R:Chachaya, K.R.; Shapiro, R.; Riordan, J.F.; Vallee, B.L.
Proc. Natl. Acad. Sci. U.S.A. 92, 2949-2953, 1995
A:Title: Crystal structure of bovine angiotensin at 1.5 Angstroms resolution.
A:Reference number: A58315; MUID:95224057
A:Contents: annotation; X-ray crystallography, 1.5 angstroms
R:Lequin, O.; Albarot, C.; Bontems, F.; Spik, G.; Lallemand, J.Y.
submitted to the Brookhaven Protein Data Bank, April 1996
A:Reference number: A65709; PDB:1G10
A:Contents: annotation; conformation by (1)H-NMR, residues 1-125
R:Lequin, O.; Albarot, C.; Bontems, F.; Spik, G.; Lallemand, J.Y.
Biochemistry 35, 8870-8880, 1996
A:Title: Solution structure of bovine angiotensin by (1)H nuclear magnetic resonance spect

```

Oy      6  FOKHLL-----TNTRDVDCNIIIM-STNLF--HCKDKNTFTISRPREPKAICCKTIASKNV  57
          |:::|      |:::|      |:::|      |:::|      |:::|      |:::|
Db      8  FERQHMDSRGSPPNPNPYCNEMMKSRMMTQGRCKRPVNTFHEEPRLADYQAVC---FQKNV  63

Oy      58  L-----TTSEFYLSDCNVTSPRP---CKYKLEKSTNTFCVTCENQ--APVHF  98
          |:::|      |:::|      |:::|      |:::|      |:::|      |:::|
Db      64  LCKNGQNCYQNSNMMHITDCRVTSNSDYPRNCVSRTOEQEKSIYVAAEGNYPVYVHF  120

RESULT  10

NRMKH
pancreatic ribonuclease (EC 3.1.27.5) - minke whale
N:Alternate names: RNase 1; RNase A
C:Species: Balaeoptera acutirostrata (minke whale, lesser rorqual)
C:Date: 24-Apr-1984 #sequence_revision 24-Apr-1984 #text_change 03-Jun-1994
C:Accession: A00818

R:Emmens, M.; Welling, G.W.; Beintema, J.J.
Biochem. J. 157, 317-323, 1976
#:Title: The amino acid sequence of pike whale (lesser rorqual) pancreatic ribonuclease

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A:Reference number: A00818; MWID:76277855
A:Accession: A00818
A:Molecule type: protein
A:Residues: 1-124 <EMM>
C:Superfamily: pancreatic ribonuclease
C:Keywords: glycoprotein; hydrolase; nucleic acid digestion; pancreas
F.12_41,119/Active site: His, Lys, His #status predicted
F.26-84,40-95,58-110,65-72/disulfide bonds: #status predicted
F.76/Binding site: carbohydrate (Asn) (covalent) (partial) #status experimental

Query Match 21.2%; Score 122; DB 1; Length 124;
Best Local Similarity 28.6%; Pred. No. 1.5e-05;
Matches 34; Conservative 15; Mismatches 42; Indels 28; Gaps 6;

QY 4 LTFQKKHLNTRDQVD-----CNITMSTNLF--HCKQKNTFYSPREPYAICKGIITASK 55
:|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db 6 MKRQRQHMDSGNSPGNNPNYCNOQMRRKMTQGCKRPYNTFVHSLDEYKAVC-----SOK 61
:|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|

QY 56 NVL-----TTSEFLSDCNVTSRP-----CKYKLKSTNFCYVCENQ--APVHF 98
:|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db 62 NVLCKNGRFTNCYESNSTMHTIDCRQTQSSKYPNCAYVTSQKEKHIIYACEGNPYVPVHF 120
:|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|

RESULT 11
NRKS
pancreatic ribonuclease (EC 3.1.27.5) - casiragua
C:Species: Proechimys guairae (casiragua)
C:Date: 17-Mar-1987 #sequence_revision 17-Mar-1987 #text_change 30-Sep-1993
C:Accession: A00821
-R.Belintema, J.J.; Knol, G.; Martena, B.
Biochim. Biophys. Acta 705, 102-110, 1982
A:Title: The primary structures of pancreatic ribonucleases from African porcine and
A:Reference number: A90644; MWID:83000399
A:Accession: A00821
A:Molecule type: protein
A:Residues: 1-128 <BEI>
A:Note: Residues 67-78 were positioned primarily by homology with other ribonucleases
C:Superfamily: pancreatic ribonuclease
C:Keywords: glycoprotein; hydrolase; nucleic acid digestion; pancreas
F.12_41,119/Active site: His, Lys, His #status predicted
F.26-84,40-95,58-110,65-72/disulfide bonds: #status predicted
F.34/Binding site: carbohydrate (Asn) (covalent) #status experimental

Query Match 21.0%; Score 121; DB 1; Length 128;
Best Local Similarity 29.9%; Pred. No. 2.5e-05;
Matches 35; Conservative 18; Mismatches 36; Indels 28; Gaps 7;

QY 6 FOKKHL-----TTRDQDCNIM--STNLF--HCKDKNTFYSPREPYAICKGIITASKNV 57
:|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db 8 FOKHIDSSGSPNTNPYCNAMKSRMNTQERCKPNTFVEHPLADVAVC---FQKNV 63
:|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|

QY 58 -----LTTSEFLSDCNVTSR-----PCKYKLKSTNFCYVCENQ--APVHF 98
:|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db 64 PCKNGSNCYESTSNMHTIDCRILTSNSKFPDCLVLTSTQSEKSIIVACGNGPYVPVHF 120
:|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|

RESULT 12
A35932
angiotenin precursor - mouse
N:Alternate names: angiotenesis factor
N:Contains: ribonuclease (EC 3.1.27.-)
C:Species: Mus musculus (house mouse)
C:Date: 09-Nov-1990 #sequence_revision 09-Nov-1990 #text_change 18-Jun-1999
C:Accession: A35932
R:Bond, M.D.; Vallee, B.L.
Biochem. Biophys. Res. Commun. 171, 988-995, 1990
A:Title: Isolation and sequencing of mouse angiotenin DNA.
A:Reference number: A35932; MWID:91025023
A:Accession: A35932
A:Status: not compared with conceptual translation
A:Molecule type: DNA

```

A:Residues: 1-145 <BON>
A:Cross-references: GB:U22516; NID:g726325; PIDN:AAA91366.1; PID:g726326
C:Genetics:
A:Introns: #status absent
C:Function:
A:Description: hydrolyzes tRNA; induces vascularization of normal and malignant tissue
C:Superfamily: pancreatic ribonuclease
C:Keywords: angiotensin; hydrolyase; nucleic acid degradation; pyroglutamic acid
E:1-24/Domain: signal sequence #status predicted <IG>
E:25-145/Product: angiotensin #status predicted <MA>
F:25/Modified site: pyrrolidone carboxylic acid (Gln) (in mature form) #status predicted
F:37-64/13/Active site: His, Lys, His #status predicted
F:50-104, 63-115, 81-130/Disulfide bonds: #status predicted

Query Match	20.6%	Score 118.5	DB 1	Length 145
Best Local Similarity	35.5%	Pred. 0.5.le-05		
Matches	27	Conservative 11	Mismatches 31	Indels 7
				Gaps 3
Qy	30	CKDKNTFTYSRPEPKAIC--KGIATKNV-LTTSFYLDSDCNVTS---RPCKYKLKKS	82	
		: : : : : :		
Db	63	CKDVTFTFHGKNSNKAICGANGSPYRENLNRKSKSPFOVTTCKHGTGSPRPCCQIRASAG	122	
Qy	83	TNTFCVTCEQAPVHF	98	
		:		
Db	123	PRHYIVACENGLPVHF	138	

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RESULT      13
NRPP
pancreatic ribonuclease (EC 3.1.27.5) - pig
N.Alternate names: RNase I; RNase A
C.Species: Sus scrofa domestica (domestic pig)
C.Date: 24-Apr-1984 #sequence_revision 24-Apr-1984 #text-change 03-Jun-1994
C.Accession: A92071; A93191; A00816
R.Jackson, R.L.; Hirs, C.H.W.
J. Biol. Chem. 245, 637-653, 1970
A.Title: The primary structure of porcine pancreatic ribonuclease. II. The amino acid
A.Reference number: A92071; MUID:70104197
A.Accession: A92071
A.Molecule type: protein
A.Residues: 1,'Q','3-124 <JNC>
R.Merenga, R.K.; Huizinga, J.D.; Gaestera, W.; Welling, G.W.; Beintema, J.J.
FEBS Lett. 31, 181-185, 1973
A>Title: Affinity chromatography of porcine pancreatic ribonuclease and reinvestigati
A.Reference number: A91391
A.Accession: A91391
A.Molecule type: protein
A.Residues: 1-124 <WIE>
R.Pheilan, J.J.; Hirs, C.H.W.
J. Biol. Chem. 245, 654-661, 1970
A>Title: The primary structure of porcine pancreatic ribonuclease. III. The disulfide
A.Reference number: A92072; MUID:70104198
A.Contents: annotation: disulfide bonds
C.Superfamily: pancreatic ribonuclease
C.Keywords: glycoprotein; hydrolase; nucleic acid digestion; pancreas
F:12,41,119/Active site: His, Lys, His #status predicted
F:21,34,76/Binding site: carbohydrate (Asn) (covalent) #status experimental
F:26-84,40-95,58-110,65-72/Disulfide bonds: #status experimental

Query Match          20.3%: Score 117; DB 1; Length 124;
Best Local Similarity 29.9%; Pred. No. 6.2e-05;
Matches 35; Conservative 14; Mismatches 40; Indels 28; Gaps 7;

OY      6 FOKKHLFTTRPVD-----CNININSTNF--HCKDKNTFYTSRPDYKAICKGI-I 52
       ||::||| | |::||| | |::||| | |::||| | |::||| | |::||| | |::|||
DB      8 FORQHLM---DPDSSSSNSNYCNILMSRRMTGGRCPVPTVEHESLADVOAVCSQIIV 63
       ||::||| | |::||| | |::||| | |::||| | |::||| | |::|||

OY      53 ASKNVL-----TSEFIYSDCNVTSRP----CKTKLKSTTFPCVTEENO--APVHF 98
       ||::||| | |::||| | |::||| | |::||| | |::||| | |::|||
DB     64 NCKNGQINCVCOSNSTHTTDCROGTGGSKRYPCAIFKASODCKHIIITVADEGNPVYVHE 120
       ||::||| | |::||| | |::||| | |::||| | |::||| | |::|||

```

RESULT 14

152489

ribonuclease 4 (EC 3.1.-.-) precursor - human

N:Alternate names: RNase 4

C:Species: Homo sapiens (man)

C>Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 22-Jun-1999

C/Accession: 152489 #sequence: S60163; S38272

R:Geno. M.: Futami, J.; Tashima, Y.; Akutagawa, K.; Kosaka, M.; Tada, H.; Yamada, H.

Biochim. Biophys. Acta 1261, 424-426, 1995

A>Title: Molecular cloning and expression of human ribonuclease 4 cDNA.

A:Reference number: 152489; MUID:95260866

A/Accession: 152489

A>Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-147 <RES>

A/Cross-references: GB:D37931; NID:9976228; PIDN:BA07150.1; PID:9976229

R:Nosenberg, H.F.; Dyer, K.D.

Nucleic Acids Res. 23, 4290-4295, 1995

A>Title: Human ribonuclease 4 (RNase 4): coding sequence, chromosomal localization and

A:Reference number: S60163; MUID:96091174

A/Accession: S60163

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 29-53, 'D', 55-147 <ROS>

A/Cross-references: EMBL:U36775; NID:91040977; PIDN:AAA96750.1; PID:91040978

R:Zhou, H.M.; Strydom, D.J.

Eur. J. Biochem. 217, 401-410, 1993

A>Title: The amino acid sequence of human ribonuclease 4, a highly conserved ribonuclease

A:Reference number: S38272; MUID:94039064

A/Accession: S38272

A:Molecule type: protein

C:Genetics: 29-147 <ZHO>

A:Gene: GDB:RNASE4

A/Cross-references: GDB:6108046; OMIM:601030

A:Map position: 14q24-q31

A:Introns: #status absent

C:Superfamily: pancreatic ribonuclease

C:Keywords: hydrolase

F:40,68,144/active site: His, Lys, His #status predicted

F:53-109,67-120,85-135,92-99/disulfide bonds: #status predicted

Query Match

Best Local Similarity 32.1%; Score 116.5; DB 2; Length 147;

Matches 36; Conservative 16; Mismatches 43; Indels 17; Gaps 7;

RESULT 15

B43825

angiotensin - rabbit

C:Species: Oryctolagus cuniculus (domestic rabbit)

C>Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999

C/Accession: S29833; B43825

R:Bond, M.D.; Strydom, D.J.; Vallee, B.L.

Biochim. Biophys. Acta 1162, 177-186, 1993

A>Title: Characterization and sequencing of rabbit, pig and mouse angiotensins: discernme

A:Reference number: S29833; MUID:93192291

A/Accession: S29833

A>Status: preliminary

A:Molecule type: protein

A:Residues: 1-125 <BON>

A>Note: submitted to the Protein Sequence Database, December 1992

C:Superfamily: pancreatic ribonuclease

C:Keywords: pyroglutamic acid
F:1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental

Query Match

Best Local Similarity 31.2%; Score 116; DB 1; Length 125;

Matches 24; Conservative 13; Mismatches 32; Indels 8; Gaps 3;

Query 30 CKDKNTFIYSRPEPKAICK---GIISKNV-LTTFSEFLSDCNVTS---RPCKYKLUK 81

Db 39 CKDTNFTVHGKSGIKDVCEDKNGKPYGKNFRISKSSFQVTTCKHVGSGPWPDPYRATS 98

Query 82 STNFTCVTCENQAPVHF 98

Db 99 GSRNIVVIACENGLPVHF 115

Search completed: August 9, 2002, 20:05:08
Job time: 136 sec

